

Package ‘LDheatmap’

April 17, 2009

Title Graphical display of pairwise linkage disequilibria between SNPs

Version 0.2-7

Author Ji-Hyung Shin <shin@sfu.ca>, Sigal Blay <sblay@sfu.ca>, Nicholas Lewin-Koh <nikko@hailmail.net>, Brad McNeney <mcneney@stat.sfu.ca>, Jinko Graham <jgraham@stat.sfu.ca>

Description Produces a graphical display, as a heat map, of measures of pairwise linkage disequilibria between SNPs. Users may optionally include the physical locations or genetic map distances of each SNP on the plot.

Maintainer Ji-Hyung Shin <shin@sfu.ca>

Depends R (>= 2.0.0), grid

Imports genetics

License GPL-2

URL <http://stat-db.stat.sfu.ca:8080/statgen/research/LDheatmap/>

Repository CRAN

Date/Publication 2009-01-14 18:11:42

R topics documented:

CEUData	2
CHBJPTData	3
LDheatmap	4
LDheatmap.highlight	9
LDheatmap.marks	10
Index	12

CEUData

Example data set for LDheatmap

Description

CEUSNP: Genotypes on 15 SNPs for 60 people

CEUDist: Physical map positions of the 15 SNPs in CEUSNP

Usage

```
data(CEUData)
```

Format

CEUSNP: A dataframe of SNP genotypes. Each row represents an individual. Each column represents a SNP.

CEUDist: A vector of integers, representing SNP physical map locations on the chromosome.

Details

Data on SNPs with minor allele frequency greater than 5% from a 9kb region of chromosome 7 (base positions 126273659 through 126282556 from release 7 of the International HapMap Project). Genotypes from 30 parent-offspring trios (both parents, one offspring) were obtained. The 30 trios are taken from the so-called CEPH families, a set of multi-generational families from Utah with ancestry from northern and western Europe. From this set of 90 people, 60 parents were extracted.

Source

International HapMap Project www.hapmap.org

References

The International HapMap Consortium. A haplotype map of the human genome. *Nature* 437, 1299-1320. 2005.

Examples

```
data(CEUData)
```

`CHBJPTData`*Example data set for LDheatmap*

Description

CHBJPTSNP: Genotypes on 13 SNPs for 45 Chinese and 45 Japanese people

CHBJPTDist: Physical map positions of the 13 SNPs

Usage

```
data(CHBJPTData)
```

Format

CHBJPTSNP: A dataframe of SNP genotypes. Each row represents an individual. Each column represents a SNP.

CHBJPTDist: a vector of integers, representing SNP physical map locations on the chromosome.

Details

The data frame `CHBJPTSNP` contains genotypes for 13 SNPs on chromosome 7, from 45 Chinese and 45 Japanese individuals. The Chinese individuals were unrelated residents of the community at Beijing Normal University with at least 3 Han Chinese grandparents. The Japanese individuals were unrelated residents of the Tokyo metropolitan area with all grandparents from Japan. The data are from release 21 of the International HapMap project (The International HapMap Consortium 2005).

Source

International HapMap Project www.hapmap.org

References

The International HapMap Consortium. A haplotype map of the human genome. *Nature* 437, 1299-1320. 2005.

Examples

```
data(CHBJPTData)
#Now do our panel plot with LDheatmaps in the panels
library(lattice)
pop<-factor(c(rep("chinese", 45), rep("japanese", 45)))
xyplot(1~1|pop,pch=" ", scales=list(draw=FALSE),xlab="",ylab="")
trellis.focus("panel",1,1)
LDheatmap(CHBJPTSNP[pop=="chinese",],CHBJPTDist,newpage=FALSE)
trellis.focus("panel",2,1)
LDheatmap(CHBJPTSNP[pop=="japanese",],CHBJPTDist,newpage=FALSE)
```

LDheatmap

*This function produces a pairwise LD plot.***Description**

LDheatmap() is used to produce a graphical display, as a heat map, of pairwise linkage disequilibrium (LD) measurements for SNPs. The heat map is a false color image in the upper-left diagonal of a square plot. Optionally, a line parallel to the diagonal of the image indicating the physical or genetic map positions of the SNPs may be added, along with text reporting the total length of the genomic region considered.

Usage

```
LDheatmap(gdat, genetic.distances=NULL, distances="physical",
          LDmeasure="r", title="Pairwise LD", add.map=TRUE, add.key=TRUE,
          geneMapLocation=0.15, geneMapLabelX=0.5, geneMapLabelY=0.3,
          SNP.name=NULL, color=grey.colors(20), newpage=TRUE,
          name="ldheatmap", vp.name=NULL, pop=FALSE)
```

Arguments

gdat	SNP data: a data frame of genotype objects, a square matrix of pairwise linkage disequilibrium measurements or an object of class "LDheatmap" (the returned object of this function).
genetic.distances	A numeric vector of map locations of the SNPs, in the same order as SNPs listed in gdat, in terms of genetic or physical distances. Physical distances should be in bases, genetic distances should be in centiMorgans (cM). When gdat is <i>not</i> an object of class LDheatmap, the default is a vector that represents equi-spaced markers, 1kb (1000 bases) apart. When gdat <i>is</i> an object of class LDheatmap, the genetic.distances argument is taken to be the genetic.distances list item of gdat.
distances	A character string to specify whether the provided map locations are in physical or genetic distances. If distances="physical" (default), the text describing the total length of the region will be "Physical Length:XXkb" where XX is the length of the region in kilobases. If distances="genetic", the text will be "Genetic Map Length:YYcM" where YY is the length of the region in centiMorgans. If gdat is an object of class LDheatmap, distances is taken from gdat.
LDmeasure	A character string specifying the measure of LD - either allelic correlation r^2 or Lewontin's $ D' $; default = "r" for r^2 ; type "D'" for $ D' $. This argument is ignored when the user has already supplied calculated LD measurements through gdat (i.e., when gdat is a matrix of pairwise LD measurements or an object of class "LDheatmap").
title	A character string for the main title of the plot. Default is "Pairwise LD".

<code>add.map</code>	If TRUE (default), a diagonal line indicating the physical or genetic map positions of the SNPs will be added to the plot, along with text indicating the total length of the genetic region.
<code>add.key</code>	If TRUE (default) the color legend is drawn.
<code>geneMapLocation</code>	A numeric value specifying the position of the line parallel to the diagonal of the matrix; the larger the value, the farther it lies from the matrix diagonal. Ignored when <code>add.map=FALSE</code> .
<code>geneMapLabelX</code>	A numeric value specifying the x-coordinate of the text indicating the total length of the genomic region being considered. Ignored when <code>add.map=FALSE</code> .
<code>geneMapLabelY</code>	A numeric value specifying the y-coordinate of the text indicating the total length of the genomic region being considered. Ignored when <code>add.map=FALSE</code> .
<code>SNP.name</code>	A vector of character string(s) of SNP name(s) to be labelled. Should match the names of SNPs in the provided object <code>gdat</code> , otherwise nothing is done.
<code>color</code>	A range of colors to be used for drawing the heat map. Default is <code>grey.colors(20)</code> .
<code>newpage</code>	If TRUE (default), the heat map will be drawn on a new page.
<code>name</code>	A character string specifying the name of the LDheatmap graphical object (<code>grob</code>) to be produced.
<code>vp.name</code>	A character string specifying the name of the viewport where the heat map is going to be drawn.
<code>pop</code>	If TRUE, the viewport where the heat map is drawn is popped (i.e. removed) from the viewport tree after drawing. Default=FALSE.

Details

For `gdat`, any square matrix with values between 0 and 1 inclusive can be passed, and the values above the diagonal will be plotted. In the display of LD, SNPs appear in the order supplied by the user as the horizontal and vertical coordinates are increased and one moves along the off-diagonal line, from the bottom-left to the top-right corner. To achieve this, the conventions of the `image()` function have been adopted, in which horizontal coordinates correspond to the rows of the matrix and vertical coordinates correspond to columns, and vertical coordinates are indexed in increasing order from bottom to top.

For the argument `color`, an appropriate color palette for quantitative data is recommended, as outlined in the help page of the `brewer.pal()` function of the **RColorBrewer** package.

See the package vignette, of the same name as the package, for more details.

Value

An object of class "LDheatmap" which contains the following components:

<code>LDmatrix</code>	The matrix of pairwise LD measurements plotted in the heat map.
<code>LDheatmapGrob</code>	A grid graphical object (<code>grob</code>) representing the produced heat map.
<code>heatmapVP</code>	The viewport in which the heat map is drawn. See viewport .

`genetic.distances` The vector of the supplied physical or genetic map locations, or the vector of equispaced marker distances when no distance vector is supplied.

`distances` A character string specifying whether the provided map distances are physical or genetic.

The grob `LDheatmapGrob` has three grobs as its children (components). They are listed below along with their own children and respectively represent the color image with main title, genetic map and color key of the heat map:

```
"heatMap" - "heatmap", "title";
"geneMap" - "diagonal", "segments",
"titles", "symbols", "SNPnames"; and
"Key" - "colorKey", "title", "labels",
"ticks", "box".
```

Note

The produced heat map can be modified in two ways. First, it is possible to edit *interactively* the grob components of the heat map, by using the function `grid.edit`; the function will not work if there is no open graphical device showing the heat map. Alternatively, the user can use the function `editGrob` and work with the grob `LDheatmapGrob` returned by `LDheatmap`. See Examples for usage.

`LDheatmap()` uses `Grid`, which does not respond to `par()` settings. Hence modifying `par()` settings of `mfgrow` and `mfcoll` will not work with `LDheatmap()`. The Examples section shows how to display multiple heat maps on one plot without the use of `par()`.

Author(s)

Ji-hyung Shin <shin@sfu.ca>, Sigal Blay <sblay@sfu.ca>, Nicholas Lewin-Koh <nikko@hailmail.net>, Brad McNeney <mcneney@stat.sfu.ca>, Jinko Graham <jgraham@cs.sfu.ca>

References

Shin J-H, Blay S, McNeney B and Graham J (2006). LDheatmap: An R Function for Graphical Display of Pairwise Linkage Disequilibria Between Single Nucleotide Polymorphisms. *Journal of Statistical Software*, **16** Code Snippet 3

See Also

[LD](#), [genotype](#), [grid](#), [LDheatmap.highlight](#), [LDheatmap.marks](#)

Examples

```
#Load the package's data set
data(CEUData)
#Creates a data frame "CEUSNP" of genotype data and a vector "CEUDist"
#of physical locations of the SNPs
```

```

##### Produce a heat map in a grey color scheme #####

MyHeatmap <- LDheatmap(CEUSNP, genetic.distances = CEUDist,
  color = grey.colors(20))

# Prompt the user before starting a new page of graphics output
# and save the original prompt settings in old.prompt.
old.prompt <- devAskNewPage(ask = TRUE)

# Highlight a certain LD block of interest:
LDheatmap.highlight(MyHeatmap, i = 3, j = 8, col = "black", fill = "grey" )
# Plot a symbol in the center of the pixel which represents LD between
# the fourth and seventh SNPs:
LDheatmap.marks(MyHeatmap, 4, 7, gp=gpar(cex=2), pch = "*")

##### Modify the plot by using 'grid.edit' function #####
#Draw a heat map where the SNPs "rs2283092" and "rs6979287" are labelled.
LDheatmap(MyHeatmap, SNP.name = c("rs2283092", "rs6979287"))

#Find the names of the top-level graphical objects (grobs) on the current display
getNames()
#[1] "ldheatmap"

# Find the names of the component grobs of "ldheatmap"
childNames(grid.get("ldheatmap"))
#[1] "heatMap" "geneMap" "Key"

#Find the names of the component grobs of heatMap
childNames(grid.get("heatMap"))
#[1] "heatmap" "title"

#Find the names of the component grobs of geneMap
childNames(grid.get("geneMap"))
#[1] "diagonal" "segments" "title" "symbols" "SNPnames"

#Find the names of the component grobs of Key
childNames(grid.get("Key"))
#[1] "colorKey" "title" "labels" "ticks" "box"

#Change the plotting symbols that identify SNPs rs2283092 and rs6979287
#on the plot to bullets
grid.edit("symbols", pch = 20, gp = gpar(cex = 1))

#Change the color of the main title
grid.edit(gPath("ldheatmap", "heatMap", "title"), gp = gpar(col = "red"))

#Change size of SNP labels
grid.edit(gPath("ldheatmap", "geneMap", "SNPnames"), gp = gpar(cex=1.5))

#Add a grid of white lines to the plot to separate pairwise LD measures
grid.edit(gPath("ldheatmap", "heatMap", "heatmap"), gp = gpar(col = "white",
  lwd = 2))

```

```

##### Modify a heat map using 'editGrob' function #####
MyHeatmap <- LDheatmap(MyHeatmap, color = grey.colors(20))

new.grob <- editGrob(MyHeatmap$LDheatmapGrob, gPath("geneMap", "segments"),
                    gp=gpar(col="orange"))

##Clear the old graphics object from the display before drawing the modified heat map:
grid.newpage()

grid.draw(new.grob)
# now the colour of line segments connecting the SNP
# positions to the LD heat map has been changed from black to orange.

##### Draw a resized heat map (in a 'blue-to-red' color scale #####
grid.newpage()

pushViewport(viewport(width=0.5, height=0.5))
LDheatmap(MyHeatmap, SNP.name = c("rs2283092", "rs6979287"), newpage=FALSE,
           color="blueToRed")
popViewport()

##### Draw and modify two heat maps on one plot #####
grid.newpage()

##Draw and the first heat map on the left half of the graphics device
pushViewport(viewport(x=0, width=0.5, just="left"))
LD1<-LDheatmap(MyHeatmap, color=grey.colors(20), newpage=FALSE,
               title="Pairwise LD in grey.colors(20)",
               SNP.name="rs6979572", geneMapLabelX=0.6,
               geneMapLabelY=0.4, name="ld1")
upViewport()

##Draw the second heat map on the right half of the graphics device
pushViewport(viewport(x=1,width=0.5,just="right"))
LD2<-LDheatmap(MyHeatmap, newpage=FALSE, title="Pairwise LD in heat.colors(20)",
               SNP.name="rs6979572", geneMapLabelX=0.6, geneMapLabelY=0.4, name="ld2")
upViewport()

##Modify the text size of main title of the first heat map.
grid.edit(gPath("ld1", "heatMap", "title"), gp=gpar(cex=1.5))

##Modify the text size and color of the SNP label of the second heat map.
grid.edit(gPath("ld2", "geneMap", "SNPnames"), gp=gpar(cex=1.5, col="DarkRed"))

##### Draw a lattice-like plot with heat maps in panels #####
# Load CHBJP_TSNP and CHBJP_TDist
data(CHBJP_TData)
# Make a variable which indicates Chinese vs. Japanese
pop <- factor(c(rep("chinese",45), rep("japanese",45)))
library(lattice)

xyplot(1:nrow(CHBJP_TSNP) ~ 1:nrow(CHBJP_TSNP) | pop,
       type="n", scales=list(draw=FALSE), xlab="", ylab="")

```

```

panel=function(x, y, subscripts,...) {
  LDheatmap(CHBJP[SNP[subscripts,]], CHBJPTDist, newpage=FALSE) })

#Reset the user's setting for prompting on the graphics output
#to the original value before running these example commands.
devAskNewPage(old.prompt)

```

LDheatmap.highlight

Highlight a genetic region in the linkage disequilibrium heat map

Description

The function `LDheatmap.highlight()` is used to highlight a specified genetic region in the linkage disequilibrium (LD) heat map drawn with the `LDheatmap()` function.

Usage

```
LDheatmap.highlight(LDheatmap, i, j, fill = "NA", col = "black", lwd = 1, lty = 1)
```

Arguments

<code>LDheatmap</code>	An object of class "LDheatmap" returned by the function <code>LDheatmap()</code> .
<code>i</code>	A numeric value specifying the index of the first SNP to be in the highlighted region.
<code>j</code>	A numeric value specifying the index of the last SNP, which must be different from <code>i</code> , to be in the highlighted region.
<code>fill</code>	Color to fill the highlighted area with.
<code>col</code>	A character string specifying the color of the line segments defining the boundary of highlighted region; see <code>par()</code> for possible values.
<code>lwd</code>	A <i>positive</i> number specifying the width of the boundary segments.
<code>lty</code>	Either an integer or a character string specifying the line type of the boundary segments; see <code>par()</code> for possible values.

Value

A data frame of the x and y coordinates of points defining the border of the highlighted area.

Warning

By default, `LDheatmap.highlight()` finds the viewport to draw on from the `LDheatmap` object passed to it as an argument. However, if `LDheatmap()` was called with the option `pop=TRUE`, the resulting `LDheatmap` object is not assigned a viewport. In this case, `LDheatmap.highlight()` assumes the user wishes to highlight in the current viewport. Therefore, if `LDheatmap()` has been called with the option `pop=TRUE`, the user must navigate to the correct viewport before calling `LDheatmap.highlight()`.

Note

The function `LDheatmap.highlight()` highlights the cells representing the pairwise LD for the SNPs located between *i*-th and *j*-th (inclusive) SNPs in the genomic region of interest. The order of indices has no effect on the plot. For example, `LDheatmap.highlight(LDheatmap, i=2, j=4)` is the same as `LDheatmap.highlight(LDheatmap, i=4, j=2)`, which highlights the cells representing the pairwise LD for the second, third and fourth SNPs.

Author(s)

Nicholas Lewin-Koh <nikko@hailmail.net>, Ji-Hyung Shin <shin@sfu.ca>, Sigal Blay <sblay@sfu.ca>

Examples

```
data(CEUData)
tt <- LDheatmap(CEUSNP, genetic.distances=CEUDist)
LDheatmap.highlight(tt, 3, 8, col="blue", fill="green", lwd=3)
```

LDheatmap.marks *Plots a symbol in the centers of cells of the heat map image*

Description

The function `LDheatmap.marks()` is used to plot a symbol in the centers of cells representing the pairwise linkage disequilibria of specified pairs of SNPs.

Usage

```
LDheatmap.marks(LDheatmap, i, j = NULL, pch = 20, gp=gpar(...), ...)
```

Arguments

<code>LDheatmap</code>	An object of class "LDheatmap" returned by the function <code>LDheatmap()</code> .
<code>i</code>	A vector of indices of the first set of SNPs.
<code>j</code>	A vector of indices of the second set of SNPs.
<code>pch</code>	Either an integer value or a single character specifying the symbol to be plotted. See <code>points()</code> for possible values and their corresponding symbols.
<code>gp</code>	Graphical parameters; See <code>gpar()</code> .
<code>...</code>	Graphical parameter settings to be passed on to the <code>gpar()</code> function.

Details

The lengths of the vectors i and j must be the same and greater than or equal to 1. If the lengths are greater than 1, the function plots the specified symbol in the centers of the (i^k, j^k) -th cells (for $k=1, \dots, K$; $K = \text{length of the vectors } i \text{ and } j$), where i^k and j^k are the k -th elements of vectors i and j , respectively. For example, if $i=c(1, 2)$ and $j=c(3, 5)$, `LDheatmap()` plots a symbol in the centers of the cells representing pairwise linkage disequilibria between the first and third SNPs and between the second and fifth SNPs in the genome of interest. Note that the order of the sets of indices does not matter; for example, `LDheatmap.marks(LDheatmap, i=c(1, 2), j=c(3, 5))` is equivalent to `LDheatmap.marks(LDheatmap, i=c(3, 5), j=c(1, 2))`.

Value

<code>x</code>	The vector of x coordinate(s) of the plotted symbol(s).
<code>y</code>	The vector of y coordinate(s) of the plotted symbol(s).

Warning

By default, `LDheatmap.marks()` finds the viewport to draw on from the `LDheatmap` object passed to it as an argument. However, if `LDheatmap()` was called with the option `pop=TRUE`, the resulting `LDheatmap` object is not assigned a viewport. In this case, `LDheatmap.marks()` assumes the user wishes to highlight in the current viewport. Therefore, if `LDheatmap()` has been called with the option `pop=TRUE`, the user must navigate to the correct viewport before calling `LDheatmap.marks()`.

Author(s)

Nicholas Lewin-Koh <nikko@hailmail.net>, Ji-Hyung Shin <shin@sfu.ca>, Sigal Blay <sblay@sfu.ca>

Examples

```
data(CEUData)
tt <- LDheatmap(CEUSNP, genetic.distances=CEUDist)
LDheatmap.marks(tt, 15, 3, cex=1.6, col="blue")
```

Index

*Topic **aplot**

LDheatmap.highlight, 9

LDheatmap.marks, 10

*Topic **datasets**

CEUData, 2

CHBJPTData, 3

*Topic **hplot**

LDheatmap, 4

brewer.pal, 5

CEUData, 2

CEUdist (CEUData), 2

CEUSNP (CEUData), 2

CHBJPTData, 3

CHBJPTdist (CHBJPTData), 3

CHBJPTSNP (CHBJPTData), 3

editGrob, 6

genotype, 6

gpar, 10

Grid, 6

grid, 6

grid.edit, 6

hapmapCEU (CEUData), 2

hapmapCHB (CHBJPTData), 3

hapmapJPT (CHBJPTData), 3

LD, 6

LDheatmap, 4, 9, 10

LDheatmap.highlight, 6, 9

LDheatmap.marks, 6, 10

par, 9

points, 10

viewport, 5